SEP 1 6 2004

SEQUENCE LISTING

DEGUSSA AG <120> NOVEL NUCLEOTIDE SEQUENCES CODING FOR THE POXB GENE 021123-0265182 <130> <140> US 09/456,306 1999-12-08 <141> <150> DE 199 51 975.7 <151> 1999-10-28 <160> 5 <170> PatentIn version 3.3 <210> 1 <211> 2160 <212> DNA <213> Corynebacterium glutamicum <220> <221> -35 signal <222> (227)..(232) <220> <221> -10_signal (256)..(261) <222> <220> <221> CDS <222> (327)..(2063) <400> ttagaggcga ttctgtgagg tcactttttg tggggtcggg gtctaaattt ggccagtttt 60 cgaggcgacc agacaggcgt gcccacgatg tttaaatagg cgatcggtgg gcatctgtgt 120 ttggtttcga cgggctgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaaagt 180 gggcatccct gtttggtacc gagtacccac ccgggcctga aactccctgg caggcgggcg 240 aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaacac 300 353 aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta Met Ala His Ser Tyr Ala Glu Gln Leu 401 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile gag tgg gtg cac gtt cga aat gag gaa gcg gcg ttt gca gcc ggt 497 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly 50 45

	Glu			act Thr										545
				cac His										593
				ttg Leu 95	-		-	-					_	641
		_	_	ttc Phe	_	_	_		_	_		_		689
				tgc Cys										737
				gcg Ala										785
_		_		cct Pro		_		_	_	_	_	_	 _	833
				tcc Ser 175									ttc Phe 185	881
			Thr	gct Ala										929
				ttc Phe										977
				gcg Ala	Glu								gcg Ala	1025
				tac Tyr										1073
				ggt Gly 255										1121
				cta Leu	-		-	_						1169
				gtt Val										1217

	-	-		-	gtg Val	_		-			_	_	_	1265
					ttg Leu									1313
		-			ctç Leu 335								gtg Val 345	1361
_		_			cat His		_		_					1409
					att Ile									1457
					ggc Gly									1505
					acg Thr									1553
					ttg Leu 415								gat Asp 425	1601
					atc Ile									1649
					ctg Leu									1697
_					aac Asn									1745
					cca Pro									1793
					gcg Ala 495								acc Thr 505	1841
					cgc Arg						Ala			1889
		_	_		gat Asp		-	-	_		 _			1937

			gga ttc agc aag Gly Phe Ser Lys 550	
acc cga acc gtc Thr Arg Thr Val 555	ttt ggt gga Phe Gly Gly 560	Gly Val Gly	gcg atg atc gat Ala Met Ile Asp 565	ctg gcc 2033 Leu Ala
cgt tcg aac ata Arg Ser Asn Ile 570			tgatgattga tacad	cetget 2083
gttctcattg accg	cgagcg cttaa	ctgcc aacatt	tcca ggatggcagc t	cacgccggt 2143
gcccatgaga ttgc	cct			2160
<210> 2 <211> 579 <212> PRT <213> Coryneba	cterium glut	amicum		
<400> 2				
Met Ala His Ser 1	Tyr Ala Glu 5	Gln Leu Ile 10	Asp Thr Leu Glu	Ala Gin 15
Gly Val Lys Arg 20	Ile Tyr Gly	Leu Val Gly 25	Asp Ser Leu Asn 30	Pro Ile
Val Asp Ala Val 35	Arg Gln Ser	Asp Ile Glu 40	Trp Val His Val	Arg Asn
Glu Glu Ala Ala 50	Ala Phe Ala 55.	Ala Gly Ala	Glu Ser Leu Ile 60	Thr Gly
Glu Leu Ala Val 65	Cys Ala Ala 70	Ser Cys Gly	Pro Gly Asn Thr 75	His Leu 80
Ile Gln Gly Leu	Tyr Asp Ser 85	His Arg Asn 90	Gly Ala Lys Val	Leu Ala 95
Ile Ala Ser His		Ala Gln Ile 105	Gly Ser Thr Phe	Phe Gln
Glu Thr His Pro 115	Glu Ile Leu	Phe Lys Glu 120	Cys Ser Gly Tyr 125	Cys Glu
Met Val Asn Gly 130	Gly Glu Gln 135		Ile Leu His His	Ala Ile
Gln Ser Thr Met 145	Ala Gly Lys 150	Gly Val Ser	Val Val Val Ile 155	Pro Gly 160
Asp Ile Ala Lys	Glu Asp Ala 165	Gly Asp Gly 170	Thr Tyr Ser Asn	Ser Thr 175
Ile Ser Ser Gly 180		Val Phe Pro 185	Asp Pro Thr Glu 190	Ala Ala
Ala Leu Val Glu 195	Ala Ile Asn	Asn Ala Lys 200	Ser Val Thr Leu 205	Phe Cys

- Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu 210 215 220
- Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile 225 230 235 240
- Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr 245 250 255
- Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Leu 260 265 .270
- Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala 275 280 285
- Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys 290 295 300
- Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro 305 310 315 320
- His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys 325 330 335
- Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn 340 345 350
- Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu 355 360 365
- Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met 370 380
- Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg 385 390 395 400
- Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro 405 410 415
- His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala 420 425 430
- Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr 435 440 445
- Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Phe Asn Asn Ser 450 455 460
- Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu 465 470 475 480
- Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala 485 490 495
- Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu 500 505 510
- Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile 515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu 530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly 545 550 555 560

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile 565 570 575

Pro Thr Pro

<210> 3

<211> 875

<212> DNA

<213> Corynebacterium glutamicum

<400> 3

tgcgagatgg tgaatggtgg tgagcagggt gaacgcattt tgcatcacgc gattcagtcc accatggcgg gtaaaggtgt gtcggtggta gtgattcctg gtgatatcgc taaggaagac 120 graggtgacg gtacttattc caattccact atttcttctg gractcctgt ggtgttcccg 180 gatectactg aggetgeage getggtggag gegattaaca acgetaagte tgteactttg 240 ttctgcggtg cgggcgtgaa gaatgctcgc gcgcaggtgt tggagttggc ggagaagatt 300 aaatcaccga tcgggcatgc gctgggtggt aagcagtaca tccagcatga gaatccgttt 360 420 gaggteggea tgtetggeet gettggttae ggegeetgeg tggatgegte caatgaggeg gatctgctga ttctattggg tacggatttc ccttattctg atttccttcc taaagacaac 480 gttgcccagg tggatatcaa cggtgcgcac attggtcgac gtaccacggt gaagtatccg 540 600 gtgaccggtg atgttgctgc aacaatcgaa aatattttgc ctcatgtgaa ggaaaaaaca 660 gategtteet teettgateg gatgeteaag geacaegage gtaagttgag eteggtggta gagacgtaca cacataacgt cgagaagcat gtgcctattc accctgaata cgttgcctct 720 attttgaacg agctggcgga taaggatgcg gtgtttactg tggataccgg catgtgcaat 780 gtgtggcatg cgaggtacat cgagaatccg gagggaacgc gcgactttgt gggttcattc 840 cgccacggca cgatggctaa tgcgttgcct catgc 875

<220>

<223> Primer

<400> 4

tgcgagatgg tgaatggtgg

<210> 4

<211> 20

<212> DNA

<213> Artificial

<210> 5
<211> 20
<212> DNA
<213> Artificial
<220>
<223> Primer

<400> 5 gcatgaggca acgcattagc

20